



## SEQUENCE LISTING

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KIKUCHI, Kaoru

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<141> 1999-06-09

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ggggagcacc gaggttgggt ccaagacata gagtcagcag atgtctcctc tttgtgtcct 1140
aaagagcctg gagaacgtcc agtagtgttt gaagttcccg tggctacagc tgcgcatgtg 1200
gtcttgccat gttctccaag ctacgcatgg gcatcctgtg tgtggcacca gccagtgga 1260
gtgactgcac tcaccccccg gcgggatgga ctggaggtgg tggtgacccc agggggccatg 1320
ggcgcttatg cctgtgaatg tcaggagggg ggggcagccc atgtggtagc agcttacagc 1380
ttggtatggg gcagccagcg agatgctccg agccggggcc acacagtggg ggcgggactg 1440
gctggcttct tcttggggat tctcgcagca tccctgactc tcattctgat tggtcggcgt 1500
cagcagcgac ggcgacagag ggaacttctg gctagagaca aggtgggcct ggacctgggg 1560
gctccacctt ctgggaccac aagctacagc caagaccctc cctccccctc tcctgaagat 1620
gagcggttgc cgctggccct ggccaagagg ggcagtggct ttggtggatt ctcaccaccc 1680
ttcctgcttg atccttgccc aagcccagcc cacattcggc taactggggc tcctctagcc 1740
acatgtgatg aaacatccat c 1761
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<210> 6

<211> 587

<212> PRT

<213> Homo sapiens

<400> 6

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 1          5          10          15
Pro Ile Ile Thr Arg Ala Val Gly Arg Ala Glu Asp Trp Ile Arg Thr
 20          25          30
Asp Thr Leu Pro Ser Trp Leu Asn Ala Pro Ala Phe Val Ala Ala Val
 35          40          45
Ala Leu Ser Pro Ala Glu Trp Gly Asp Glu Asp Gly Asp Asp Glu Ile
 50          55          60
Tyr Phe Phe Phe Thr Glu Thr Ser Arg Ala Phe Asp Ser Tyr Glu Arg
 65          70          75          80
Ile Lys Val Pro Arg Val Ala Arg Val Cys Ala Gly Asp Leu Gly Gly
 85          90          95
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Arg	Lys	Thr	Leu	Gln	Gln	Arg	Trp	Thr	Thr	Phe	Leu	Lys	Ala	Asp	Leu	
			100					105					110			
Leu	Cys	Pro	Gly	Pro	Glu	His	Gly	Arg	Ala	Ser	Ser	Val	Leu	Gln	Asp	
			115					120					125			
Val	Ala	Val	Leu	Arg	Pro	Glu	Leu	Gly	Ala	Gly	Thr	Pro	Ile	Phe	Tyr	
			130					135					140			
Gly	Ile	Phe	Ser	Ser	Gln	Trp	Glu	Gly	Ala	Thr	Ile	Ser	Ala	Val	Cys	
															160	
Ala	Phe	Arg	Pro	Gln	Asp	Ile	Arg	Thr	Val	Leu	Asn	Gly	Pro	Phe	Arg	
															175	
Glu	Leu	Lys	His	Asp	Cys	Asn	Arg	Gly	Leu	Pro	Val	Val	Asp	Asn	Asp	
															190	
Val	Pro	Gln	Pro	Arg	Pro	Gly	Glu	Cys	Ile	Thr	Asn	Asn	Met	Lys	Leu	
															205	
Arg	His	Phe	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Asp	Arg	Val	Leu	Thr	Phe	
															220	
Ile	Arg	Asp	His	Pro	Leu	Met	Asp	Arg	Pro	Val	Phe	Pro	Ala	Asp	Gly	
															240	
His	Pro	Leu	Leu	Val	Thr	Thr	Asp	Thr	Ala	Tyr	Leu	Arg	Val	Val	Ala	
															255	
His	Arg	Val	Thr	Ser	Leu	Ser	Gly	Lys	Glu	Tyr	Asp	Val	Leu	Tyr	Leu	
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Gly	Thr	Glu	Asp	Gly	His	Leu	His	Arg	Ala	Val	Arg	Ile	Gly	Ala	Gln	
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Leu	Ser	Val	Leu	Glu	Asp	Leu	Ala	Leu	Phe	Pro	Glu	Pro	Gln	Pro	Val	
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Glu	Asn	Met	Lys	Leu	Tyr	His	Ser	Trp	Leu	Leu	Val	Gly	Ser	Arg	Thr	
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Glu	Val	Thr	Gln	Val	Asn	Thr	Thr	Asn	Cys	Gly	Arg	Leu	Gln	Ser	Cys	
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Ser	Glu	Cys	Ile	Leu	Ala	Gln	Asp	Pro	Val	Cys	Ala	Trp	Ser	Phe	Arg	
															350	
Leu	Asp	Glu	Cys	Val	Ala	His	Ala	Gly	Glu	His	Arg	Gly	Leu	Val	Gln	
															365	
Asp	Ile	Glu	Ser	Ala	Asp	Val	Ser	Ser	Leu	Cys	Pro	Lys	Glu	Pro	Gly	
															380	
Glu	Arg	Pro	Val	Val	Phe	Glu	Val	Pro	Val	Ala	Thr	Ala	Ala	His	Val	
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Val	Leu	Pro	Cys	Ser	Pro	Ser	Ser	Ala	Trp	Ala	Ser	Cys	Val	Trp	His	
															415	
Gln	Pro	Ser	Gly	Val	Thr	Ala	Leu	Thr	Pro	Arg	Arg	Asp	Gly	Leu	Glu	
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Val	Val	Val	Thr	Pro	Gly	Ala	Met	Gly	Ala	Tyr	Ala	Cys	Glu	Cys	Gln	
															445	
Glu	Gly	Gly	Ala	Ala	His	Val	Val	Ala	Ala	Tyr	Ser	Leu	Val	Trp	Gly	
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Ser	Gln	Arg	Asp	Ala	Pro	Ser	Arg	Ala	His	Thr	Val	Gly	Ala	Gly	Leu	
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Ala	Gly	Phe	Phe	Leu	Gly	Ile	Leu	Ala	Ala	Ser	Leu	Thr	Leu	Ile	Leu	
															495	
Ile	Gly	Arg	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Arg	Glu	Leu	Leu	Ala	Arg	
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Asp	Lys	Val	Gly	Leu	Asp	Leu	Gly	Ala	Pro	Pro	Ser	Gly	Thr	Thr	Ser	
															525	
Tyr	Ser	Gln	Asp	Pro	Pro	Ser	Pro	Ser	Pro	Glu	Asp	Glu	Arg	Leu	Pro	
															540	
Leu	Ala	Leu	Ala	Lys	Arg	Gly	Ser	Gly	Phe	Gly	Gly	Phe	Ser	Pro	Pro	



545                      550                      555                      560  
 Phe Leu Leu Asp Pro Cys Pro Ser Pro Ala His Ile Arg Leu Thr Gly  
                          565                      570                      575  
 Ala Pro Leu Ala Thr Cys Asp Glu Thr Ser Ile  
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 <211> 196  
 <212> DNA  
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<220>  
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 <222> (1)..(196)  
 <223> Coding region

<220>  
 <221> misc\_feature  
 <222> (1)..(196)  
 <223> strandedness: double

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 caagacatag agtcag 196

<210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer used to obtain the sequence encoding the intracellular domain of Semaphorin W

<400> 8  
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<210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Anti-sense PCR primer sequence used to obtain the sequence encoding the intracellular domain of Semaphorin W

<400> 9  
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<210> 10  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(333)  
 <223> Coding region

<220>  
 <221> misc\_feature  
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 <223> strandedness: double

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 tctgaggctg acttctgtct caccgggttc gcagtccttc acacatacaa ttactctgtt 180  
 ctcttgtgg atcctgcctc ccacacactt tatgttggcg cccgggacac catcttcgct 240  
 ttatccctgc ccttctcagg ggagagaccc cgcaggattg actggatggt tcctgaggct 300  
 cacagacaga actgtaggaa gaaaggcaag aaa 333

<210> 11  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
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 Leu Leu Ala Val Leu Ser Gly Pro Val Ser Gly Arg Val Pro Arg Ser  
 20 25 30  
 Val Pro Arg Thr Ser Leu Pro Ile Ser Glu Ala Asp Phe Cys Leu Thr  
 35 40 45  
 Arg Phe Ala Val Pro His Thr Tyr Asn Tyr Ser Val Leu Leu Val Asp  
 50 55 60  
 Pro Ala Ser His Thr Leu Tyr Val Gly Ala Arg Asp Thr Ile Phe Ala  
 65 70 75 80  
 Leu Ser Leu Pro Phe Ser Gly Glu Arg Pro Arg Arg Ile Asp Trp Met  
 85 90 95  
 Val Pro Glu Ala His Arg Gln Asn Cys Arg Lys Lys Gly Lys Lys  
 100 105 110

<210> 12  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Gln Asp Pro Val Cys Ala Trp  
 1 5

<210> 13  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature

<222> (1)..(1)  
<223> Xaa = Gln or Arg

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> Xaa = Ala or Gly

<400> 13  
Xaa Asp Pro Tyr Cys Xaa Trp  
1 5

<210> 14  
<211> 14  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: Myc tag

<400> 14  
Asp Ile Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
1 5 10

<210> 15  
<211> 364  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(364)  
<223> sequence of GenBank Accession No: T09073

<220>  
<221> misc\_feature  
<222> (1)..(364)  
<223> any n is a, g, c, t, unknown, or other

<400> 15  
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acnaactgtg gccgtctcca gagctgtcca gaggatccac tggcccagga cccagtctgt 120  
gcctggagct tccggctgga tgagtgtgtg gcccatgccg gggagcaccg agggttggtc 180  
caagacatag agtcagcaga tgtctcctct ttgtgtccta aagagcctgg agaacgtcca 240  
gtagtgtttg aagttcccgt ggctacagnt gcgcattgtg tcttncatg ttctccaagc 300  
tcagcatggg catcctgtgt gtggcaccag cccagtggag ttacttcact tccccccggg 360  
cggg 364